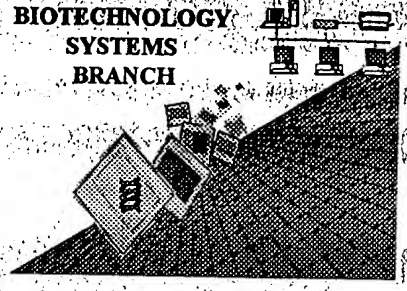
0500

BIOTECHNOLOGY SYSTEMS BRANCH



# RAW SEQUENCE LISTING ERROR REPORT

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:**

Application Serial Number: 09/513,999

Art Unit / Team No.: OIPE

Date Processed by STIC: 3/16/2000

**THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.**

**PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:**

**1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,**

**2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY**

**THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.**

**IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:**

MARK SPENCER 703-308-4212

# Raw Sequence Listing Error Summary

**ERROR DETECTED** **SUGGESTED CORRECTION** SERIAL NUMBER: 09/513,999

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

1 ____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 ____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 ____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 ____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 ____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 ____ Variable Length
Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.

7 ____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.

8 ____ Skipped Sequences (OLD RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
**(2) INFORMATION FOR SEQ ID NO:X:**
**(i) SEQUENCE CHARACTERISTICS:**(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
**(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:**
**This sequence is intentionally skipped**

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 ____ Skipped Sequences (NEW RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
**<210> sequence id number**
**<400> sequence id number**
**000**

10 ✓ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 ____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

15-16 (maybe more)

12 ✓ Use of <220>Feature (NEW RULES)
Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
**Please explain sourc of genetic material in <220> t <223> section.**
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

13 ____ PatentIn ver. 2.0 "bug"
**Please d not use "Copy t Disk" function of PatentIn version 2.0.** This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, pleas us "File Manager" or any other means to copy file t floppy disk.

AKS-Biotechnology Systems Branch- 5/15/99

**RAW SEQUENCE LISTING**
PATENT APPLICATION **US/09/513,999**

DATE: 03/16/2000
TIME: 12:39:26

Input Set: **I513999.RAW**

**This Raw Listing contains the General Information Section and those Sequences containing ERRORS.**

Does Not Comply
Corrected Diskette Needed

```
   1  <110> Dumas Milne Edwards, J.B.
   2        Duclert A.
   3        Giordano, J.Y.
   4  <120> Expressed Sequence Tags and Encoded Human Proteins.
   5  <130> GENSET.054A
   6  <150> US 60/122,487
   7  <151> 1999-02-26
   8  <160> 36681
   9  <170> Patent.pm
```

Due to size of listing, the following pages show a sample of global error. Please check all sequences to ensure <211> values match actual number of bases/amino acids shown.

**ERRORED SEQUENCES FOLLOW**

```
  10  <210> 8
E-->11  <211> 681 (227 shown)
  12  <212> PRT
  13  <213> Homo sapiens
  14  <220>
  15  <221> SIGNAL
  16  <222> -22..-1
  17  <223> score 8.5
  18        seq AALLLGLMMVVTG/DE
  19  <400> 8
  20        Met Gly Trp Thr Met Arg Leu Val Thr Ala Ala Leu Leu Leu Gly Leu
  21              -20                 -15                 -10
  22        Met Met Val Val Thr Gly Asp Glu Asp Glu Asn Ser Pro Cys Ala His
  23            -5                  1                   5                  10
  24        Glu Ala Leu Leu Asp Glu Asp Thr Leu Phe Cys Gln Gly Leu Glu Val
  25                        15                  20                  25
  26        Phe Tyr Pro Glu Leu Gly Asn Ile Gly Cys Lys Val Val Pro Asp Cys
  27                    30                  35                  40
  28        Asn Asn Tyr Arg Gln Lys Ile Thr Ser Trp Met Glu Pro Ile Val Lys
  29                45                  50                  55
  30        Phe Pro Gly Ala Val Asp Gly Ala Thr Tyr Ile Leu Val Met Val Asp
  31            60                  65                  70
  32        Pro Asp Ala Pro Ser Arg Ala Glu Pro Arg Gln Arg Phe Trp Arg His
  33        75                  80                  85                  90
  34        Trp Leu Val Thr Asp Ile Lys Gly Ala Asp Leu Lys Lys Gly Lys Ile
  35                        95                  100                 105
  36        Gln Gly Gln Glu Leu Ser Ala Tyr Gln Ala Pro Ser Pro Pro Ala His
  37                    110                 115                 120
  38        Ser Gly Phe His Arg Tyr Gln Phe Phe Val Tyr Leu Gln Glu Gly Lys
  39                125                 130                 135
```

```
40          Val Ile Ser Leu Leu Pro Lys Glu Asn Lys Thr Arg Gly Ser Trp Lys
41              140                 145                 150
42          Met Asp Arg Phe Leu Asn Arg Phe His Leu Gly Glu Pro Glu Ala Ser
43          155                 160                 165                 170
44          Thr Gln Phe Met Thr Gln Asn Tyr Gln Asp Ser Pro Thr Leu Gln Ala
45                          175                 180                 185
46          Pro Arg Glu Arg Ala Ser Glu Pro Lys His Lys Asn Gln Ala Glu Ile
47                      190                 195                 200
48          Ala Ala Cys
49                  205
```

---

```
50      <210> 10
E--> .  51  <211> 507 169 shown
52      <212> PRT
53      <213> Homo sapiens
54      <220>
55      <221> SIGNAL
56      <222> -88..-1
57      <223> score 6.7
58            seq VFALSSFLNKASA/VY
59      <400> 10
60            Met Lys Gly Gly Ile Ser Asn Val Trp Phe Asp Arg Phe Lys Ile Thr
61                        -85                 -80                 -75
62            Asn Asp Cys Pro Glu His Leu Glu Ser Ile Asp Val Met Cys Gln Val
63                    -70                 -65                 -60
64            Leu Thr Asp Leu Ile Asp Glu Glu Val Lys Ser Gly Ile Lys Lys Asn
65                -55                 -50                 -45
66            Arg Ile Leu Ile Gly Gly Phe Ser Met Gly Gly Cys Met Ala Met His
67            -40                 -35                 -30                 -25
68            Leu Ala Tyr Arg Asn His Gln Asp Val Ala Gly Val Phe Ala Leu Ser
69                            -20                 -15                 -10
70            Ser Phe Leu Asn Lys Ala Ser Ala Val Tyr Gln Ala Leu Gln Lys Ser
71                        -5                  1                   5
72            Asn Gly Val Leu Pro Glu Leu Phe Gln Cys His Gly Thr Ala Asp Glu
73                10                  15                  20
74            Leu Val Leu His Ser Trp Ala Glu Glu Thr Asn Ser Met Leu Lys Ser
75            25                  30                  35                  40
76            Leu Gly Val Thr Thr Lys Phe His Ser Phe Pro Asn Val Tyr His Glu
77                            45                  50                  55
78            Leu Ser Lys Thr Glu Leu Asp Ile Leu Lys Leu Trp Ile Leu Thr Lys
79                        60                  65                  70
80            Leu Pro Gly Glu Met Glu Lys Gln Lys
81                    75                  80
```

---

```
82      <210> 12
E--> .  83  <211> 981 327
84      <212> PRT
85      <213> Homo sapiens
86      <220>
87      <221> SIGNAL
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                      -45                 -40                 -35
      Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro Arg Lys Cys Ser Val Phe
                  -30                 -25                 -20
      His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser Leu Leu Trp
              -15                 -10                 -5
      Leu Gln Leu Ser Cys Ser Gly Asp Val Ala Arg Ala Val Arg Gly Gln
          1               5                   10                  15
      Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys Pro Pro Glu Pro Pro
                      20                  25                  30
      Pro Glu His Trp Glu Glu Asp Ala Ser Trp Gly Pro His Arg Leu Ala
                  35                  40                  45
      Val Leu Val Pro Phe Arg Glu Arg Phe Glu Glu Leu Leu Val Phe Val
              50                  55                  60
      Pro His Met Arg Arg Phe Leu Ser Arg Lys Lys Ile Arg His His Ile
          65                  70                  75
      Tyr Val Leu Asn Gln Val Asp His Phe Arg Phe Asn Arg Ala Ala Leu
      80                  85                  90                  95
      Ile Asn Val Gly Phe Leu Glu Ser Ser Asn Ser Thr Asp Tyr Ile Ala
                      100                 105                 110
      Met His Asp Val Asp Leu Leu Pro Leu Asn Glu Glu Leu Asp Tyr Gly
                  115                 120                 125
      Phe Pro Glu Ala Gly Pro Phe His Val Ala Ser Pro Glu Leu His Pro
              130                 135                 140
      Leu Tyr His Tyr Lys Thr Tyr Val Gly Gly Ile Leu Leu Leu Ser Lys
          145                 150                 155
      Gln His Tyr Arg Leu Cys Asn Gly Met Ser Asn Arg Phe Trp Gly Trp
      160                 165                 170                 175
      Gly Arg Glu Asp Asp Glu Phe Tyr Arg Arg Ile Lys Gly Ala Gly Leu
                      180                 185                 190
      Gln Leu Phe Arg Pro Ser Gly Ile Thr Thr Gly Tyr Lys Thr Phe Arg
                  195                 200                 205
      His Leu His Asp Pro Ala Trp Arg Lys Arg Asp Gln Lys Arg Ile Ala
              210                 215                 220
      Ala Gln Lys Gln Glu Gln Phe Lys Val Asp Arg Glu Gly Gly Leu Asn
          225                 230                 235
      Thr Val Lys Tyr His Val Ala Ser Arg Thr Ala Leu Ser Val Gly Gly
      240                 245                 250                 255
      Ala Pro Cys Thr Val Leu Asn Ile Met Leu Asp Cys Asp Lys Thr Ala
                      260                 265                 270
      Thr Pro Trp Cys Thr Phe Ser
                  275
```

---

```
<210> 14
E--> <211> 1185
<212> PRT
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395 shown

```
137  <213> Homo sapiens
138  <220>
139  <221> SIGNAL
140  <222> -310..-1
141  <223> score 4.4
142        seq VLILLFSLALIIL/PS
143  <400> 14
144        Met Asp Leu Gly Ile Pro Asp Leu Leu Asp Ala Trp Leu Glu Pro Pro
145        -310                -305                -300                -295
146        Glu Asp Ile Phe Ser Thr Gly Ser Val Leu Glu Leu Gly Leu His Cys
147                        -290                -285                -280
148        Pro Pro Pro Glu Val Pro Val Thr Arg Leu Gln Glu Gln Gly Leu Gln
149                    -275                -270                -265
150        Gly Trp Lys Ser Gly Gly Asp Arg Gly Cys Gly Leu Gln Glu Ser Glu
151                -260                -255                -250
152        Pro Glu Asp Phe Leu Lys Leu Phe Ile Asp Pro Asn Glu Val Tyr Cys
153            -245                -240                -235
154        Ser Glu Ala Ser Pro Gly Ser Asp Ser Gly Ile Ser Glu Asp Ser Cys
155        -230                -225                -220                -215
156        His Pro Asp Ser Pro Pro Ala Pro Arg Ala Thr Ser Ser Pro Met Leu
157                        -210                -205                -200
158        Tyr Glu Val Val Tyr Glu Ala Gly Ala Leu Glu Arg Met Gln Gly Glu
159                    -195                -190                -185
160        Thr Gly Pro Asn Val Gly Leu Ile Ser Ile Gln Leu Asp Gln Trp Ser
161                -180                -175                -170
162        Pro Ala Phe Met Val Pro Asp Ser Cys Met Val Ser Glu Leu Pro Phe
163            -165                -160                -155
164        Asp Ala His Ala His Ile Leu Pro Arg Ala Gly Thr Val Ala Pro Val
165        -150                -145                -140                -135
166        Pro Cys Thr Thr Leu Leu Pro Cys Gln Thr Leu Phe Leu Thr Asp Glu
167                        -130                -125                -120
168        Glu Lys Arg Leu Leu Gly Gln Glu Gly Val Ser Leu Pro Ser His Leu
169                    -115                -110                -105
170        Pro Leu Thr Lys Ala Glu Glu Arg Val Leu Lys Lys Val Arg Arg Lys
171                -100                -95                 -90
172        Ile Arg Asn Lys Gln Ser Ala Gln Asp Ser Arg Arg Arg Lys Lys Glu
173            -85                 -80                 -75
174        Tyr Ile Asp Gly Leu Glu Ser Arg Val Ala Ala Cys Ser Ala Gln Asn
175        -70                 -65                 -60                 -55
176        Gln Glu Leu Gln Lys Lys Val Gln Glu Leu Glu Arg His Asn Ile Ser
177                        -50                 -45                 -40
178        Leu Val Ala Gln Leu Arg Gln Leu Gln Thr Leu Ile Ala Gln Thr Ser
179                    -35                 -30                 -25
180        Asn Lys Ala Ala Gln Thr Ser Thr Cys Val Leu Ile Leu Leu Phe Ser
181                -20                 -15                 -10
182        Leu Ala Leu Ile Ile Leu Pro Ser Phe Ser Pro Phe Gln Ser Arg Pro
183            -5                  1                   5                   10
184        Glu Ala Gly Ser Glu Asp Tyr Gln Pro His Gly Val Thr Ser Arg Asn
185                        15                  20                  25
186        Ile Leu Thr His Lys Asp Val Thr Glu Asn Leu Glu Thr Gln Val Val
```

```
187                    30                  35                  40
188         Glu Ser Arg Leu Arg Glu Pro Pro Gly Ala Lys Asp Ala Asn Gly Ser
189                45                  50                  55
190         Thr Arg Thr Leu Leu Glu Lys Met Gly Gly Lys Pro Arg Pro Ser Gly
191             60                  65                  70
192         Arg Ile Arg Ser Val Leu His Ala Asp Glu Met
193         75                  80                  85
```

---

```
194    <210> 48
E--OK  195    <211> 361
196    <212> DNA
197    <213> Homo sapiens
198    <220>
199    <221> CDS
200    <222> 63..359
201    <221> sig_peptide
202    <222> 63..119
203    <223> score 10.8
204          seq ILFLVAAATGAHS/QV
205    <400> 48
W-->   206  gagcatcacc cagcaaccac atctgtnctc tagagaatcc cctgasagct ccgttcctca   60
207          cc atg gac tgg acc tgg agg atc ctc ttc ttg gtg gca gca gcc acm      107
208             Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr
209                              -15                 -10                 -5
210          gga gcc cac tcc cag gtg crr ctg stg caa tct ggg gct gag gtg aag    155
211          Gly Ala His Ser Gln Val Xaa Leu Xaa Gln Ser Gly Ala Glu Val Lys
212                           1                   5                  10
213          arg cct ggg gcc tcw gtg aag gtc tcc tgy aag rct tct gga tac rcc    203
214
215          Xaa Pro Gly Ala Ser Val Lys Val Ser Cys Lys Xaa Ser Gly Tyr Xaa
216                  15                  20                  25
E--OK  217   ttc asc gkc tac tat ata cac tgg sts cgm cag gcc cct gga caa ggg   251
218          Phe Xaa Xaa Tyr Tyr Ile His Trp Xaa Arg Gln Ala Pro Gly Gln Gly
219              30                  35                  40
220          ctt gag tgg atg ggw cgg ats aat cct aag gat ggt gcc ccc aac tat    299
221          Leu Glu Trp Met Gly Arg Xaa Asn Pro Lys Asp Gly Ala Pro Asn Tyr
222          45                  50                  55                  60
223          gca ccg aac ttt gaa ggc agg gtc acc atg acc agg gac acg tcc atc    347
224          Ala Pro Asn Phe Glu Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile
225                           65                  70                  75
226          acc aca gcg tac at                                              361
227          Thr Thr Ala Tyr
228                           80
```

---

```
229    <210> 101
E--OK  230    <211> 722
231    <212> DNA
232    <213> Homo sapiens
233    <220>
234    <221> CDS
```

(next page)

```
      235  <222> 337..720
      236  <221> sig_peptide
      237  <222> 337..408
      238  <223> score 4.2
      239        seq IWSFPLIIAAVCA/QS
      240  <400> 101
W-->   241        agaatcagac cgaaaccnag agagacagca ttgcctttct gcgtcycctc gcccmmctcs     60
      242        sctcctgcta taaataaccc ggastagcgg gtcaggaacg tcacacggcg agaaaacagg    120
      243        accccgaggt tttcttctct gggaataggg ggcaaagggt gaggagagga gaaagaaatc    180
      244        gctcgaaatc tgctcggtcc ccggcagccg ccgcttcccc tttgacgttt tggtacgccg    240
      245        tgcgcatgcg cctcacatta gaattactgc actgggcaga ctaagttgga tctcctctct    300
      246        tcagtgaaac cctcaattcc atcaaaaact aaaggg atg tgg aga gtg cgg aaa       354
      247                                                Met Trp Arg Val Arg Lys
      248                                                                    -20
      249        arg ggc tac ttt ggg att tgg tcc ttc ccc tta ata atc gcc gct gtc      402
      250
      251        Xaa Gly Tyr Phe Gly Ile Trp Ser Phe Pro Leu Ile Ile Ala Ala Val
      252                    -15                 -10                 -5
E--OK 253        tgt gcg cag agt gtc aat gac cct agt aat atg tcg ctg gtt aaa gag      450
      254        Cys Ala Gln Ser Val Asn Asp Pro Ser Asn Met Ser Leu Val Lys Glu
      255                1               5                   10
      256        acg gtg gat aga ctc ctg aaa ggc tat gac att cgt ctg aga cca gat      498
      257        Thr Val Asp Arg Leu Leu Lys Gly Tyr Asp Ile Arg Leu Arg Pro Asp
      258        15                  20                  25                  30
      259        ttt gga ggt ccc ccc gtg gct gtg ggg atg aac att gac att gcc agc      546
      260        Phe Gly Gly Pro Pro Val Ala Val Gly Met Asn Ile Asp Ile Ala Ser
      261                        35                  40                  45
      262        atc gat atg gtt tct gaa gtc aat atg gat tat acc ttg aca atg tac      594
      263        Ile Asp Met Val Ser Glu Val Asn Met Asp Tyr Thr Leu Thr Met Tyr
      264                    50                  55                  60
      265        ttt caa caa gcc tgg aga gat aag agg ctg tct awa aat gta ata cct      642
      266        Phe Gln Gln Ala Trp Arg Asp Lys Arg Leu Ser Xaa Asn Val Ile Pro
      267                65                  70                  75
      268        tta aac ttg act ctg gac aac aga gtg gca gac cag ctc tgg gtg cct      690
      269        Leu Asn Leu Thr Leu Asp Asn Arg Val Ala Asp Gln Leu Trp Val Pro
      270            80                  85                  90
      271        gat acc tat ttc ctg aac gat aag aag tca tt                          722
      272        Asp Thr Tyr Phe Leu Asn Asp Lys Lys Ser
      273        95                  100
```

---

```
      274  <210> 2790
E-OK  275  <211> 462
      276  <212> DNA
      277  <213> Homo sapiens
      278  <220>
      279  <221> CDS
      280  <222> 42..461
      281  <400> 2790
W-->   282        agttgannaga ggccatcaag atcctggaga gcctcaagaa c atg act gtg gag cag    56
      283                                                    Met Thr Val Glu Gln
```

```
284                                                         1               5
285         ctg ctg acg ggc tcg ccc acc tct ccg act gtg gag cct gag aag cca      104
286         Leu Leu Thr Gly Ser Pro Thr Ser Pro Thr Val Glu Pro Glu Lys Pro
287                     10                  15                  20
288         act cgg gag aag aag ttt ctg gat gac atc aag aag cta cag gaa aac      152
289         Thr Arg Glu Lys Lys Phe Leu Asp Asp Ile Lys Lys Leu Gln Glu Asn
290                 25                  30                  35
291         ctc aag aag acc ctg gac aat gtg gcc att gta gag gag gag aag atg      200
292         Leu Lys Lys Thr Leu Asp Asn Val Ala Ile Val Glu Glu Glu Lys Met
293                 40                  45                  50
294         gaa gca gtg ccc gac gta gag cgc aag gag gac aag ccc gag ggg cag      248
295         Glu Ala Val Pro Asp Val Glu Arg Lys Glu Asp Lys Pro Glu Gly Gln
296             55                  60                  65
W--> 297    tca cct gtg aag gnn gag tgg ccc agc gaa acc ccg gtg ctg tgc cag      296
298         Ser Pro Val Lys Xaa Glu Trp Pro Ser Glu Thr Pro Val Leu Cys Gln
299         70                  75                  80                  85
300         cag tgt ggc ggc aag cct ggc gtc acc ttc acc agc gcc aag ggc gag      344
301         Gln Cys Gly Gly Lys Pro Gly Val Thr Phe Thr Ser Ala Lys Gly Glu
302                     90                  95                  100
303         gtc ttc tcc gta ctg gag ttt gca ccc tca aat cat tct ttt aag aaa      392
304         Val Phe Ser Val Leu Glu Phe Ala Pro Ser Asn His Ser Phe Lys Lys
305                 105                 110                 115
306         att gag ttc cag cct cca gaa gcc aag aag ttc ttc agc aca gtg cgg      440
307         Ile Glu Phe Gln Pro Pro Glu Ala Lys Lys Phe Phe Ser Thr Val Arg
308                 120                 125                 130
309         arg gag atg gcg ctg ctg gct a                                       462
310
311         Xaa Glu Met Ala Leu Leu Ala
312             135                 140
```

---

```
313   <210> 4101
E--> 314  <211> 282
315   <212> PRT
316   <213> Homo sapiens
317   <220>
318   <221> SIGNAL
319   <222> -20..-1
320   <223> score 5
321         seq LQRFAVLSRGVHS/SV
322   <400> 4101
323         Met Phe Ser Lys Leu Ala His Leu Gln Arg Phe Ala Val Leu Ser Arg
324         -20                 -15                 -10                 -5
325         Gly Val His Ser Ser Val Ala Ser Ala Thr Ser Val Ala Thr Lys Lys
326                     1                   5                   10
327         Thr Val Gln Gly Pro Pro Thr Ser Asp Asp Ile Phe Glu Arg Glu Tyr
328                 15                  20                  25
W--> 329    Lys Tyr Gly Ala His Asn Tyr Xaa Pro Leu Pro Val Ala Leu Glu Arg
330             30                  35                  40
331         Gly Lys Gly Ile Tyr Leu Trp Asp Val Glu Gly Arg Lys Tyr Phe Asp
332         45                  50                  55                  60
```

```
333          Phe Leu Ser Ser Tyr Ser Ala Val Asn Gln Gly His Cys His
334                          65                  70
```

---

```
335    <210> 4102
E--> 336    <211> 213 91
337    <212> PRT
338    <213> Homo sapiens
339    <220>
340    <221> SIGNAL
341    <222> -20..-1
342    <223> score 3.5
343          seq WQLVLNVWGKVEA/DI
344    <400> 4102
345          Met Gly Leu Ser Asp Gly Glu Trp Gln Leu Val Leu Asn Val Trp Gly
346          -20                 -15                 -10                 -5
347          Lys Val Glu Ala Asp Ile Pro Gly His Gly Gln Glu Val Leu Ile Arg
348                          1                   5                  10
349          Leu Phe Lys Gly His Pro Glu Thr Leu Glu Lys Phe Asp Lys Phe Lys
350                  15                  20                  25
351          His Leu Lys Ser Glu Asp Glu Met Lys Ala Ser Glu Asp Leu Lys Lys
352              30                  35                  40
353          His Gly Ala Thr Val Leu Thr
354          45                  50
```

---

```
355    <210> 4103
E--> 356    <211> 339 113
357    <212> PRT
358    <213> Homo sapiens
359    <220>
360    <221> SIGNAL
361    <222> -20..-1
362    <223> score 3.5
363          seq WQLVLNVWGKVEA/DI
364    <400> 4103
365          Met Gly Leu Ser Asp Gly Glu Trp Gln Leu Val Leu Asn Val Trp Gly
366          -20                 -15                 -10                 -5
367          Lys Val Glu Ala Asp Ile Pro Gly His Gly Gln Glu Val Leu Ile Arg
368                          1                   5                  10
369          Leu Phe Lys Gly His Pro Glu Thr Leu Glu Lys Phe Asp Lys Phe Lys
370                  15                  20                  25
371          His Leu Lys Ser Glu Asp Glu Met Lys Ala Ser Glu Asp Leu Lys Lys
372              30                  35                  40
373          His Gly Ala Thr Val Leu Thr Ala Leu Gly Gly Ile Leu Lys Lys Lys
374          45                  50                  55                  60
375          Gly His His Glu Ala Glu Ile Lys Pro Leu Ala Gln Ser His Ala Thr
376                          65                  70                  75
W--> 377     Lys His Lys Ile Pro Val Lys Xaa Xaa Gly Val His Leu Gly Met His
378                      80                  85                  90
379          His
```

see item 10

---

```
380    <210> 4104
```

E--> 381 <211> 324 108 shown
382 <212> PRT
383 <213> Homo sapiens
384 <220>
385 <221> SIGNAL
386 <222> -34..-1
387 <223> score 3.8
388 seq TLFVFISXGSALG/FK
389 <400> 4104
390 Met Ala Ser Glu Phe Lys Lys Lys Leu Phe Trp Arg Ala Val Val Ala
391 -30 -25 -20
W--> 392 Glu Phe Leu Ala Thr Thr Leu Phe Val Phe Ile Ser Xaa Gly Ser Ala
393 -15 -10 -5
W--> 394 Leu Gly Phe Lys Tyr Pro Val Gly Xaa Asn Gln Thr Ala Val Gln Asp
395 1 5 10
396 Asn Val Lys Val Ser Leu Ala Phe Gly Leu Ser Ile Ala Thr Leu Ala
397 15 20 25 30
398 Gln Ser Val Gly His Ile Ser Gly Ala His Leu Asn Pro Ala Val Thr
399 35 40 45
W--> 400 Leu Gly Leu Leu Leu Ser Cys Gln Ile Ser Ile Phe Arg Xaa Ser Cys
401 50 55 60
402 Thr Ser Ser Pro Ser Ala Trp Gly Pro Ser Ser Pro
403 65 70

---

404 <210> 4105
E--> 405 <211> 348 116
406 <212> PRT
407 <213> Homo sapiens
408 <220>
409 <221> SIGNAL
410 <222> -44..-1
411 <223> score 5.5
412 seq ILFFTGWWIMIDA/AV
413 <400> 4105
414 Met Ala Gly Phe Leu Asp Asn Phe Arg Trp Pro Glu Cys Glu Cys Ile
415 -40 -35 -30
416 Asp Trp Ser Glu Arg Arg Asn Ala Val Ala Ser Val Val Ala Gly Ile
417 -25 -20 -15
418 Leu Phe Phe Thr Gly Trp Trp Ile Met Ile Asp Ala Ala Val Val Tyr
419 -10 -5 1
420 Pro Lys Pro Glu Gln Leu Asn His Ala Phe His Thr Cys Gly Val Phe
421 5 10 15 20
422 Ser Thr Leu Ala Phe Phe Met Ile Asn Ala Val Ser Asn Ala Gln Val
423 25 30 35
424 Arg Gly Asp Ser Tyr Glu Ser Gly Cys Leu Gly Arg Thr Gly Ala Arg
425 40 45 50
W--> 426 Val Xaa Leu Phe Ile Gly Phe Met Leu Met Phe Gly Ser Leu Ile Ala
427 55 60 65
428 Ser Met Trp Ile
429 70

```
      430  <210> 4106
E-->  431  <211> 300 /100
      432  <212> PRT
      433  <213> Homo sapiens
      434  <220>
      435  <221> SIGNAL
      436  <222> -19..-1
      437  <223> score 6.2
      438        seq WXFLVAIIKGVQC/XX
      439  <400> 4106
W-->   440       Met Glu Phe Gly Leu Xaa Trp Xaa Phe Leu Val Ala Ile Ile Lys Gly
       441  -15                 -10                 -5
W-->   442  1 ten  Val Gln Cys Xaa Xaa Xaa Leu Val Glu Ser Gly Gly Xaa Leu Val Lys
       443  1                   5                   10
W-->   444  10     Xaa Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
       445        15                  20                  25
W-->   446       Ser Asp Xaa Tyr Met Xaa Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu
       447        30                  35                  40                  45
W-->   448       Glu Trp Val Ser Tyr Ile Ser Ser Gly Gly Xaa Tyr Thr Asn Tyr Ala
       449                  50                  55                  60
W-->   450       Asp Ser Xaa Xaa Gly Arg Xaa Xaa Ile Ser Arg Asp Asn Ala Lys Asn
       451                  65                  70                  75
       452        Ser Leu Tyr Leu
       453                 80
```

```
      454  <210> 4107
E-->  455  <211> 378 /126  see next page, too
      456  <212> PRT
      457  <213> Homo sapiens
      458  <220>
      459  <221> SIGNAL
      460  <222> -19..-1
      461  <223> score 11.7
      462        seq VFCLLAVAPGAHS/QV
      463  <400> 4107
      464        Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly
      465          \   .   .   -15                 -10                 -5
      466        Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
      467                    1                   5                   10
      468        Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
      469          15                  20                  25
W-->   470       Thr Ser Xaa Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Xaa
       471  1 ten 30                  35                  40                  45
W-->   472  10    Glu Trp Met Gly Ile Ile Asn Pro Ser Xaa Gly Ser Thr Xaa Tyr Ala
       473                  50                  55                  60
       474        Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser
       475                  65                  70                  75
W-->   476       Thr Val Tyr Met Xaa Leu Ser Ser Leu Xaa Ser Xaa Asp Thr Ala Val
       477                 80                  85                  90
```

```
W--> 478 ifen 10  Tyr Xaa Cys Ala Arg Xaa Ala Tyr Ser Ser Tyr Arg Phe Asp
     479              95                  100                 105
-------------------------------------------------------------------------
     480 <210> 4108
E--> 481 <211> 381 /127
     482 <212> PRT
     483 <213> Homo sapiens
     484 <220>
     485 <221> SIGNAL
     486 <222> -19..-1
     487 <223> score 11
     488       seq TLLLLTVPSWVLS/QV
     489 <400> 4108
     490       Met Asp Ile Leu Cys Ser Thr Leu Leu Leu Leu Thr Val Pro Ser Trp
     491                       -15                 -10                 -5
     492       Val Leu Ser Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys
     493                   1               5                  10
     494       Pro Thr Gln Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu
     495           15                  20                  25
W--> 496       Xaa Thr Ser Gly Met Xaa Val Ser Trp Ile Arg Gln Xaa Pro Gly Lys
     497 ifen 10 30                  35                  40                  45
W--> 498       Xaa Leu Glu Trp Leu Ala Xaa Ile Asp Trp Xaa Asp Asp Lys Xaa Tyr
     499                       50                  55                  60
     500       Ser Thr Ser Leu Lys Asn Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys
     501                   65                  70                  75
     502       Asn Gln Val Val Leu Thr Leu Ser Lys Met Asp Pro Val Asp Thr Ala
     503               80                  85                  90
     504       Thr Tyr Tyr Cys Ala Arg Ser Arg Leu Val Pro His Asp His Trp
     505           95                  100                 105
-------------------------------------------------------------------------
     506 <210> 4109
E--> 507 <211> 264 88
     508 <212> PRT
     509 <213> Homo sapiens
     510 <220>
     511 <221> SIGNAL
     512 <222> -19..-1
     513 <223> score 11
     514       seq TLLLLTVPSWVLS/QV
     515 <400> 4109
     516       Met Asp Ile Leu Cys Ser Thr Leu Leu Leu Leu Thr Val Pro Ser Trp
     517                       -15                 -10                 -5
W--> 518 ifen  Val Leu Ser Gln Val Thr Leu Xaa Glu Ser Gly Pro Ala Leu Val Lys
     519 10                1               5                  10
     520       Pro Thr Glu Thr Leu Thr Leu Thr Cys Thr Leu Ser Gly Phe Ser Leu
     521           15                  20                  25
     522       Asn Val Ser Gly Met Arg Met Ile Trp Val Arg Gln Phe Pro Gly Gln
     523       30                  35                  40                  45
     524       Ala Leu Glu Trp Leu Ala Arg Ile Asp Trp Asp Asp Glu Lys Tyr Phe
     525                       50                  55                  60
```

```
      526          Thr Ser Ser Leu Arg Thr Arg Leu
      527                      65
-------------------------------------------------------------------------------
      528    <210> 4110
E-->  529    <211> 330 /10
      530    <212> PRT
      531    <213> Homo sapiens
      532    <220>
      533    <221> SIGNAL
      534    <222> -19..-1
      535    <223> score 10.6
      536          seq ILFLVAAXTGAXS/QV
      537    <400> 4110
W-->  538          Met Asp Trp Thr Trp Ser Ile Leu Phe Leu Val Ala Ala Xaa Thr Gly
      539                          -15                 -10                  -5
W-->  540          Ala Xaa Ser Gln Val Xaa Leu Xaa Gln Ser Gly Xaa Glu Val Lys Xaa
      541                      1                   5                   10
W-->  542          Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Xaa Phe
      543              15                  20                  25
W-->  544          Xaa Arg Tyr Xaa Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
      545          30                  35                  40                  45
      546          Glu Trp Met Gly Trp Ile Ser Pro Tyr Asn Gly Asn Thr Asn Tyr Ala
      547                          50                  55                  60
      548          Gln Gln Phe Gln Asp Arg Val Thr Leu Thr Thr Asp Thr Ser Thr Ser
      549                      65                  70                  75
      550          Thr Ala Phe Leu Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr
      551                  80                  85                  90
-------------------------------------------------------------------------------
      552    <210> 4111
E-->  553    <211> 360 /20 (see next page, top)
      554    <212> PRT
      555    <213> Homo sapiens
      556    <220>
      557    <221> SIGNAL
      558    <222> -19..-1
      559    <223> score 10.7
      560          seq ILFLVAAATGXHS/QV
      561    <400> 4111
      562          Met Asp Trp Thr Trp Ser Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
      563                          -15                 -10                  -5
W-->  564          Xaa His Ser Gln Val Gln Leu Val Gln Ser Gly Xaa Glu Val Lys Lys
      565                      1                   5                   10
      566          Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
      567              15                  20                  25
      568          Thr Ser Tyr Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
      569          30                  35                  40                  45
W-->  570          Glu Trp Met Gly Trp Ile Ser Xaa Tyr Asn Gly Asn Thr Asn Tyr Ala
      571                          50                  55                  60
W-->  572          Gln Xaa Xaa Gln Gly Arg Val Thr Met Thr Xaa Asp Thr Ser Thr Asn
      573                      65                  70                  75
```

item 10

```
W--> 574  Thr Ala Tyr Met Xaa Leu Arg Xaa Leu Arg Ser Asp Asp Thr Ala Val
     575       80                  85                  90
W--> 576  Tyr Tyr Cys Ala Xaa Arg Gly Leu
     577  95                  100
```

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```
     578  <210> 4112
E--> 579  <211> 396
     580  <212> PRT
     581  <213> Homo sapiens
     582  <220>
     583  <221> SIGNAL
     584  <222> -19..-1
     585  <223> score 10.8
     586        seq ILFLVAAATGAHS/QV
     587  <400> 4112
     588        Met Asp Trp Thr Trp Ser Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
     589                      -15                 -10                 -5
W--> 590  Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Xaa Glu Val Lys Lys
     591                1                   5                  10
     592        Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
     593            15                  20                  25
W--> 594  Thr Xaa Tyr Xaa Ile Xaa Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
     595  30                  35                  40                  45
     596        Glu Trp Met Gly Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala
     597                      50                  55                  60
W--> 598  Gln Xaa Leu Gln Gly Arg Val Thr Met Thr Xaa Asp Thr Ser Thr Xaa
     599                65                  70                  75
W--> 600  Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Xaa
     601        80                  85                  90
W--> 602  Tyr Tyr Cys Ala Arg Glu Ile Xaa Val Xaa Xaa Cys Asp Gly Gln Leu
     603            95                  100                 105
     604        Gly Pro Gly Asn
     605        110
```

item 10

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```
     606  <210> 4113
E--> 607  <211> 315
     608  <212> PRT
     609  <213> Homo sapiens
     610  <220>
     611  <221> SIGNAL
     612  <222> -19..-1
     613  <223> score 9.5
     614        seq ILXLVAAXTGAHS/QG
     615  <400> 4113
W--> 616        Met Asp Trp Thr Trp Xaa Ile Leu Xaa Leu Val Ala Ala Xaa Thr Gly
     617                      -15                 -10                 -5
W--> 618        Ala His Ser Gln Gly Gln Xaa Val Gln Ser Gly Ala Glu Val Lys Lys
     619                1                   5                  10
W--> 620        Pro Gly Ala Ser Val Lys Val Ser Cys Lys Xaa Ser Gly Tyr Thr Phe
     621            15                  20                  25
```

Same types of errors (see next page)

FYI

**Please Note:**
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

09/513,999

<210> 15
<211> 25
<212> DNA
<213> Artificial Sequence

<400> 15
gggaagatgg agatagtatt gcctg 25

<210> 16
<211> 26
<212> DNA
<213> Artificial Sequence

<400> 16
ctgccatgta catgatagag agattc 26

Please Note:
Please ensure that all subsequent artificial/unknown sequences have a suitable explanation in the <220> - <223> section.